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October 5, 2002, 03:30:35 ; Search time 1713.89 Seconds (without alignments) 3709.145 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description  1 431.8 91.7 436 10 W72837 W72837 2d57912.11  2 403.2 85.6 432 10 W72838 W72838 2d57912.51  4 380.6 83.5 42.9 AW070916 AW070916 xa31d01.x  5 379.8 83.0 42.9 AW070916 XW070916 xa31d01.x  6 345.2 73.3 464 10 BG728312 BG728312 RS737810  8 316.8 65.8 391 10 BG728312 BG728312 RS737810  8 316.8 65.8 391 10 BG785269 BG785269/RS737810  10 308.8 65.6 403 10 R75793 RS737810  11 301.4 64.0 314 12 AS2694036 BG202313 RS721669  13 294. 65.4 313 9 AW17044 AW170044 AW340069 EST4510  14 289.4 61.4 294 9 AA340069 BE366013 BE366013 CM1.EP073  15 281 59.7 316 10 BE2926938 BE386013 CM1.EP073  16 281 59.7 316 10 BE2926938 BE366013 CM1.EP073  17 255.8 54.3 44.3 9 AL12772	Result	ų	Ouerv				<b>;-</b>
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## ALIGNMENTS

	W72837 436 ho mBNA linear per 16.00m.1006	zd57g12.rl Soares_fetal_heart_NbHH19W Homo sapiens c IMAGE:344806 5, similar to contains element MER40 re	erement ', miking sequence.		MY 2637.1 GI:1382813	EST			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	1 (bases 1 to 436)	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman	,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.	Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E. Waterston	R., Williamson, A., Wohldmann, P. and Wilson, R.	The Washu-Merck EST Project	Unpublished (1995)	Contact: Wilson RK	Washington University School of Medicine	4444 Forest Park Parkway, Box 8501. St. Louis MO 63108	Tel: 314 286 1800	Fax: 314 286 1810	Email: est@watson.wustl.edu	This clone is available rovalty-free through LLML . contact the	IMAGE Consortium (info@image.llnl.gov) for further information	Insert Length: 508 Std Error: 0.00	Seq primer: mob.REGA+ET.	Location/Qualifiers		/organism="Homo sapiens"	/db_xref-"GDB:1270181"	/db_xref="taxon:9606"	/clone="IMAGE:344806"	/clone_lib="Soares_fetal_heart_NbHH19W"	/sex="unknown"	/dev_stage="19 weeks"	/lab_host="DH10B (ampicillin resistant)"
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Email: est@watson.wustl.edu
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IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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Matches 427; Conservative
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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="BT0807"

/dev_staqe="Adult"

/note="Organ: breast; Vector: pucl8; Site_l: Smal; Site_2:
Smal; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196

/716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA amplification were performed under low
stringency conditions."
                                                                                                                                                                                                                                                                                            Homo saplens
Eukaryota, Metazoa: Chordala: Craniata; Vertebrata; Euteleosloml;
Eukaryota; Metazoa: Chordala: Catarrhini; Hominidae; Homo.
I (bases 1 to 423)
Dias Neto,E., Garcia Correa,R., Verjovski.Almeida,S., Briones,M.R.,
Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Mataukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fex: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-BT0807-041000-176-G03&t3=2000-10-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 421.
                                                                                                                                                                             BF742809
1L2-BT0807-041000-176-G03 BT0807 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF expressed Shotgun sequencing of the human transcriptome with ORF expressed
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20202663
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Pred. No. 1e-89;
0; Mismatches
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                                                AW070916 420 bp mRNA linear EST 20-OCT-2000 xa31d01.xl NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568385 3' similar to contains element TAR1 repetitive element ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. Chris Moskaluk, M.D., Ph.D., Michael R.
Technologies, Inc. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
Genome Sequencing Center
Clone distribution: NGT-GGAP clone distribution information can b
found through the I.M.A.G.E. Consortium/LLNL at:
Insert Length: 545 Std Error: 0.00
Seq primer: -400P from Gibco.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMACE:2568385"
/clone_lib="NCI_CGAP_BF18"
/fissue_type="four pooled high-grade tumors, including primary tumors and two metastatic to ovary"
/lab_host="DH108"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"/db_xref="taxon:9606"
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AW070916.1 GI:6025914
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98.1%;
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Email: scain@athersys.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                     human.
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Al139456 1 G1:3645428
EST.
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Eut@leostomi;
Mammalia: Eutheria: Primates: Catarrhini; Hominidae; Homo.
1 (bases 1 to 402)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                      240
                                                   254
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                                                                                         314
                                                                                                                    Gaps
                             101 tggtagagtgtgtccctgagatggaatcagcttgagtcttctgcaattgggtcacaacta
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                                                                                                                                                         5; Indels
                                                                                                                                                361 ttcatgcttcctgtgatttcatccaactacttaccttgcctacgata 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. 402
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1710.192"
/clone_lib="Soares_fetal_heart_NbHH19W"
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98.5%;
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Unpublished (1997)
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Matches 393; Conservative
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KEYWORDS
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ORIGIN
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TITLE
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REFERENCE

RESULT

JOURNAL.

COMMENT

FEATURES

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bG202312
RST21668 Athersys RAGE Library Homo saplens cDNA, mRNA sequence.
BG202312
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Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Caln, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Kilka, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.
Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is Hil080, since a random activation method was used, these sequence tags are not necessarily expressed in HIl080 under normal circumstances."
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                                                                                                     402 CTGGTACTCTTGGGAGTTTCCATCTATCTGGTCTCTGCCCAGAATCCGACAACAGCTGCT 343
                                                                                                                                                                                                                                         245 accactgctcgtaaagacattccagttttacccaaatgggttggggatctcccgaatggt 304
                                                                                                                                                                                                                                                                                                                                                   305 agagtgtgtccctgagatggaatcagcttgagtcttctgcaattgggtcacaactattca 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctggtactcttgggagtttccatcttctggtctctgccagaatccgacaacagctgct
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primales; Catarrhin1; Hominidae; Homo
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//db_xref="taxon:9606"
//clone_lib="Athersys RAGE Library"
//cell_line="HT1080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 464. Location/Qualifiers
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expressed in HT1080 under 103 c 67 q 104
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Bukaryota, Metazoa; Chordata; Craniata; Hominidae; Homo.

1 (bases 1 to 376)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Lerner, L., Costanco, D., McElligott, K., Boozer, S., Mays, R., Shith, R., Volsoo, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)
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Pred. No. 1.6e-78;
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3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Eax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 376.
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0; Mismatches
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&tt2-CMl-BT0738-250
Seq primer: puc 18 forward
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Email: scain@athersys.com
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[ bases 1 to 391)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays.R., Smith,J., Danzig,J. and Ducar,M.

Craation of genome-wide protein expression libraries using random activation of gene expression

Nat. Blotechnol. 19 (5), 440-445 (2001)
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3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
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// Organian="Homo sapiens"
// Ab_xref="taxon:9606"
// Clone_lib="BT0738"
// dev_stage="Adult"
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High quality sequence stop: 345.
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/do_xref="taxon:9606"
/do_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression
Libraries blotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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[ (bases 1 to 403) Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman M., M., Hullman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., R., Williamson, A., Wohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 ACCACTGCTCGTAAAGACACATTCCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agagtgtgtccctgagatggaatcagcttgagtcttctgcaattgggtcacaactattca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 TGCTTCCTGTGATTTCATCCAACTACTTACCTTGCCTACGATATCCCCTTTATCTCTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 309.8; DB 10; Length 391;
Pred. No. 2.1e-69;
0; Mismatches 8; Indels 2;
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4444 Forest Park Parkway, Box 8501, St. Louls, MO 63108
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      High quality sequence
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Contact: Greg Henkel
                                                                               Eukaryota; Metazoa;
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JOURNAL
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                                                                                                                                 REFERENCE
                                                                                                                                                      AUTHORS
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                                                                                                                                                                                                                                               1. .403
/organism="Homo sapiens"
/db_xref="Cabs.572980"
/db_xref="Cabs.572980"
/db_xref="Caxon.9606"
/clone="IMAGE:158921"
/clone="I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento Soares and M.Fatima Bonaldo."
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AZ694036
AZ694036.1 GI:11878955
                                          High quality sequence stops: 307
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 516 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 gtactcttgggagtttccatctttctggtctctgccagaatccgacaacagctgctcca 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 gctgacacgtatccagctactggtcctgatgatgatgaagcccctgatgctgaaaccact 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 actgctcgtaaagacattccagttttacccaaatgggttggggatctcccgaatgg--ta 305
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Pred. No. 3.7e-69;
0; Mismatches 15
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                                                                                                                                           Insert Length: 516 Std Error:
Seq primer: M13Rp1
High quality sequence stop: 307,
Location/Qualifiers
Email: est@watson.wustl.edu
Insert Size: 516
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ilarity 94.0%;
Conservative
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Best Local Similarity
Matches 375; Conserv
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Aurora Biosciences Corp.

Aurora Biosciences Corp.

11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584046719

Email: henkelg@aurorabio.com
Pools of cells were isolated from a GenomeScreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase
proceeded by a splice acceptor as a reporter for gene expression;
2) A promoter diving neomycin resistance followed by a splice
donor to trap downstream exons. 3' RACE from neomycin gene was
performed using total RNA from isolated pools. Output was shotgun
cloned in pAmp-1 and used to transform DH5-alpha competent
bacteria. 5' ends of reported sequences were immediately preceded
by splice donor from the trapping construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: peripheral blood; Vector: pAmp-1; 3' RACE of total RNA from genetrap pools; shotgun clone in pAmp-1 and total RNA from DH5-alpha competent bacteria."

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                                                                                               Bernardino, A.
Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo saplens"
/db_xref="taxon:9606"
/dlone_llb="Genetrap HL-60 Human Promyelocytic Leukemia
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                                                                                         Pratt, E., Huang, D., Riley, M.,
                         Mammalia; Eutheria; Primates; Catarrhin1; Hominidae;
1 (bases 1 to 314)
Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M.,
, Durick,K. and Pollok,B.
Durotxpt tags from a HL-60 GenomeScreen(TM) Library
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="acute promyelocytic leukemia"
/cell_type="promyeloblast"
/cell_line="HL-60"
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AW176044
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                  AW176044/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                         ORGANISM
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ORIGIN
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VERSION
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AUTHORS
TITLE
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SOURCE
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                                 21-APR-2001
                                                                                                                                                      1 (bases 1 to 343)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cani, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,
Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, J., Danzig, J. and Ducar, M.
J., Danzig, J. and Ducar, M.
Creation of genome-wide protein expression libraries using random activation of gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type Indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                           BG202313
RST21669 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctgcaaccaccgctgcttctaccactgctcgtaaagacattccagttttacccaaatggg 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 TTGGGGATCTCCCGAATGGTAGAGTGTCTCCCTGAGATGAGATCAGCTTGAGTCTTCTGC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aattgggtcacaactattcatgcttcctgtgatttcatccaactacttaccttgcctacg 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 299.2; DB 10;
Pred. No. 1.1e-66;
0; Mismatches 22; 1
                                                                                                                                                                                                                                                                                                                                  3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900
Fax: 216 31 9596
Fix: 2 scain@athersys.com
High quality sequence stop: 343.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
                                                                                                                                                                                                                                                                           Nat. Biotechnoí. 19 (5), 440-445 (2001)
21227151
                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                      BG202313.1 GI:13724000
                                                                                                                                                                                                                                                                                                        Contact: Scott J. Cain
Athersys, Inc.
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ilarity 93.3%;
Conservative 0
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                                                                                                     human.
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Best Local Simi
Matches 321;
                             LOCUS
DEFINITION
             BG202313/c
                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                 ORGANISM
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ORIGIN
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                                                                                                                                                           REFERENCE
                                                                                                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                            MEDLINE
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0103"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ONESTES PCR (U.S. Letters Patent application No. 196. 776 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue
      EST 16-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-BT0103-
200899-008-fila&t3=1999-08-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 313.
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AW176044 313 bp mRNA linear EST 16-NOV-199
QVO-BT0103-270899-008-f12 BT0103 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                               Enteleostomi;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                             1 (bases 1 to 313)
HGGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICH Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.4%; Score 294; DB 9; Length 313; ilarity 98.1%; Pred. No. 2.3e-65; Conservative 0; Mismatches 5; Indels
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                                                            AW176044.1 GI:6442081
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Best Local Similarity
Matches 308; Conserv
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9

DEFINITION

ACCESS 10N VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

14

RESULT 1 AA340069

14

6

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BE186013
CM1 HT0738-250400-199-bll HT0738 Homo sapiens cDNA, mRNA sequence.
BE186013
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CMI-HT0738-250
400-199-bli&t3=2000-04-25&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 4
High quality sequence stop: 316.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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/dclone_lib="HT0738"
/dov_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
Site_2: Ludwig Institute for Cancer Research)
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 316)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., Bordin,S., Costa,F.F.,
Agal,M.A., de Silva,W. Jr., Zago,M.A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
        240
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Pred. No. 5.3e-62;
0; Mismatches 5;
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93 c 71 g 82 t
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Best Local Similarity 97.8%;
Matches 306; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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1 (bases 1 to 294)

2 Adams, W.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

3 C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

4 C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

5 O., Sutton, G., Blake, J.A., Earle-Hughes, J., Fine, L.D., Fitzgerald

6 Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald

7 L.M., Fitzhugh, M.M., Fritchman, J.L., Goodhagen, N.S., Glodek, A.,

8 Chelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Naudyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bedharik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,

Welly, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon

Wenter, J.C.

Welly, J.C., Hasseltine, W.A., Fields, C., Fraser, C.M. and
                                                                                                                              21-APR-1997
Similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: arkerlav@tigr.org
for clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agtectggtaetettgggagtttecatetttetggtetetgceeagaateegacaaeage 120°;
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                                                                                                                            AA340069 294 bp mRNA linear EST EST45219 Fetal skin Homo sapiens CDNA 5' end similar to spot 2, submandibular gland protein, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="ATCC (inhost):141700"
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/clone_lib="Fetal skin"
/tissue_type="epithelium"
/cell_type="epithelial cell"
/dev_stage="fetus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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Location/Qualifiers
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Bioinformatics
                                                                                                                                                                                               AA340069.1 G1:1992307
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CTTTCAAATAAATA
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Best Local Simil
Matches 290; C
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    38 agcagtcctggtactcttggqagtttccatctttctggtctc-tgcccagaatccgacaa 116
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Sequence 15, Appl Sequence 20, Appl Sequence 20, Appl Sequence 1, Appl 1 Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 21, Appl Sequence 22, Appl Sequence 22, Appl 1

15, 20, 20, 20, 20, 20,

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1 ctttgaagcattttgtctgtgtccctgatcttcaggtcaccaccatgaagttcttagc
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Pred. No. 8.6e-126;
0; Mismatches 6;
US-08-194-087-15
PCT-US93-04648-15
US-08-770-379-20
US-08-770-379-20
US-08-757-669A-20
US-08-1820-170A-20
US-09-055-699-20
US-09-055-699-20
US-09-055-699-21
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Patent No. 6312922

GENERAL INFORMATION

APPLICANT: Dumas Milne Edwards, Jean-Baptiste

APPLICANT: Dumas Milne Edwards, Jean-Baptiste

APPLICANT: Bougueleret, Lydie

TITLE OF INVENTION: Complementary DNAS

FILE REFERENCE: GENSET.021A

CURRENT APPLICATION NUMBER: US/09/247,155A

CURRENT FILING DATE: 1999-02-09

EARLIER PRILING DATE: 1998-02-09

EARLIER PRILING DATE: 1998-04.13

EARLIER FILING DATE: 1998-04.13

EARLIER FILING DATE: 1998-04.13

EARLIER FILING DATE: 1998-04.13

EARLIER FILING DATE: 1998-08-10

EARLIER FILING DATE: 1998-08-10

EARLIER APPLICATION NUMBER: 60/099,273

EARLIER APPLICATION NUMBER: 60/099,273

SOFTWARE: PALENT DATE: 1998-10-04

NUMBER OF SEQ ID NOS: 182

SEQ ID NO 41

LENGTH: 497
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US-08-910-925-2
US-08-232-463-14
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FEATURE:
FEATURE:
LOCATION: 68..337
LOCATION: 68..337
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 68..124
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 10
OTHER INFORMATION: seq LVLGVSIFLVSA/ON
FEATURE:
NAME/KEY: polya_signal
LOCATION: 462..467
FEATURE:
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Best Local Similarity 98.5%;
Matches 463; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: 482.497
US-09-247-155-41
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US-08-194-088B-15
                         GenCore version 4.5
Copyright (c) 1993 - 2000 Com
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match 1
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Maximum DB :
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APPLICANT: Dong Kyu JIN
APPLICANT: Dong Kyu JIN
TITLE OF INVENTION: Diagnostic Method and Kit for Neuropsychiatric Diseases
TITLE OF INVENTION: Using Trinucleotide Repeats Sequence
FILE REFERENCE: 1942/36
FILE REFERENCE: 1942/36
CURRENT APPLICATION NUMBER: US/09/253,691
CURRENT FILING DATE: 1990-02-26
EARLIER FILING DATE: 1996-02-26
NUMBER OF SEQ ID NOS: 3
SOFTWARE: WordPerfect 6.1/Windows
                    aaccactgctgctgcaacaactgcgaccactgctgctcctaccactgcaaccaccgctgc 240
                                                                                                                     75 tgggagtttccatcttctggtctctgcccagaatccgacaacagctgctccagctgaca 134
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61.5%; Pred. No. 1.9e-11;
iive 0; Mismatches 69;
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US-09-253-691-3/C
Sequence 3, Application US/09253691
Patent No. 6124100
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Matches 110; Conservative
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: ORGANISM: human
US-09-253-691-3
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US-09-135-994-1/C
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Sequence 1, Application US/09135994A

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Sequence 3, Application US/08469802B

Sequence 3, Application US/08469802B

Sequence 10. 5741645

GENERAL INFORMATION:
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Minq-Yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Fatent No. 5741645

FORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: 119 No. 5741645th Fourth Street, Suite 203

STATE: MInneapolis
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ranum et al.
TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REFERENCE: University of Minnesota
CURRENT APPLICATION NUMBER: US/09/135, 994A
CURRENT FILING DATE: 1998-08-18
EARLIER FILING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    Score 65.4; DB 4;
Pred. No. 1.9e-10;
0; Mismatches 56;
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REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1225
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                    13.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 63.9%
                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens US-09-135-994-1
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                                                                                                                                                                                                                                                       LENGTH: 477
TYPE: DNA
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13.8%; Score 65; DB 2; 11.01arity 58.5%; Pred. No. 1.7e-10; Conservative 0; Mismatches 80
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/062,443
FILING DATE: 14 MAY 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/971,094
FILING DATE: 30-0CT-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,830
FILING DATE: 27-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/805,093
FILING DATE: 11-DEC-91
ATTORNEY/AGENT INFORMATION:
WANTER PARTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS
SOFWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,559
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REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0855
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 29, Application US/08320559; Patent No. 5633135; GENERAL INFORMATION:
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ADDRESSEE: Woodcock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ttctaccactgct 253
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OPERATING SYSTEM: F
SOFTWARE: WORDPERFE
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                                                                                                         Similarity
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                                                                          Query Match
Best Local Simi
Matches 113;
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                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Orr, Harry T.
APPLICANT: Chung, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Coghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
PATCAL NO. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCE: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      13.8%; Score 65; DB 1; Length 234; 58.5%; Pred. No. 1.7e-10; tive 0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE TO TAKE TO THE TOTAL T
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Sequence 3, Application US/08267803B
: Patent No. 5834183
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                         Ouery Match 13.8
Best Local Similarity 58.5
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 ttctaccactgct 253
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: MOLECULE TYPE: DNA
US-08-469-8028-3
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US-08-267-803B-3/C
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APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                         3: Woodcock Washburn Kurtz Mackiewicz 6 No. 5633135ris
One Liberty Place - 46th Floor
Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (215) 568-3100
TELEFAX: (215) 568 3439
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3376 base pairs
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Sequence 29, Application PC/TUS9404496
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Croce, Carlo
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 caccatgaagttettagcagteetggtaetettgggagttteeatetttetggleletge 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 ccagaatccgacaacagctgctccagctgacacgtatccagctactggtcctgctgatga 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             784 GAGGCTTTGAAAAACTGGTACTACTGCTGCTGCTGCTGCTACTGCTGCTGCTGCTACTGC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 tgaagcccctgatgctgaaaccactgctgctgcaacaactgcgaccactgctgctcctac 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Woodcock, Washburn, Kurtz, Macklewitz
ADDRESSEE: Norris
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Pred. No. 8.5e-10;
0; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: One Liberty Place, 46th floor CITY: Philadelphia
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,094
FILING DATE: 30-CCT-1992
PRIOR APPLICATION UNDER: US 07/888,839
FILING DATE: 27-MAY-1992
PRIOR APPLICATION NUMBER: US 07/805,093
FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INFORMATION:
REGISTATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TU-1262
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.8%; 57.4%;
                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 3376 base pairs
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Best Local Similarity 57.4%
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION:
US-08-545-860D-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POPOLOGY:
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APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli
TILE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                         103 ccagaatccgacaacagctgctccagctgacacgtatccagctactggtcctgctgatga 162
                                                                                                                                                                                                                                                                                                                                                                                                                784 GAGGCTTTGAAAAACTGGTACTACTGCTGCTGCTGCTACTGCTGCTGCTACTGCTACTGC 725
                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                              13.8%; Score 64.8; DB 1; Length 3376; 57.4%; Pred. No. 8.5e-10;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz & ADDRESSEE: No. 6040140ris
STREET: One Liberty Place, 46th floor
CITY: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,860D
FILING DATE: 07-MAR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/327,392
FILING DATE: 19-007-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/320,559
FILING DATE: 11-007-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE: 22-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-545-860D-29/c
: Sequence 29, Application US/08545860D
: Patent No. 6040140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           664 TACTGCTGCTGCTGCTGCTGC 641
                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                    Best Local Similarity 57.4
Matches 117; Conservative
  TYPE: nucleic acid
STRANDEDNESS: double
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PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                      ; NAME/KEY; CDS
; LOCATION: 196..1902
US-08-320-559-29
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Length 3376; Indels

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89 tttctggtctctgcccagaatccgacaacagctgctccagctgacacgtatccagctact 148
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                                                                                                   APPLICANT: Orr, Harry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Coghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.5%; Score 63.4; DB 1; Length 168; ilarity 63.4%; Pred. No. 4.4e-10; Conservative 0; Mismatches 56; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, STREET: 119 No. 5741645th Fourth Street, Suite 203 CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Type 1 and Method for Diagnosis NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110.00030101
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08469802B Patent No. 5741645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Mueting, Ann M. 33,977
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       612-305-1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 168 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        612-305-1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                        RESULT 10
US-08-469-802B-4/c
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Best Local Simi
Matches 97;
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Patent No. 6251589
GENERAL INCORMATION:
APPLICANT: TSUJI, Shoji
APPLICANT: SANPEI, Kazujiro
TITLE OF INVENTION: Primers Therefor
TITLE OF INVENTION: Primers Therefor
TITLE OF INVENTION: NUMBER: US/09/043,303
CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT FILING DATE: 1998-05-18
EARLIER PILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 caccatgaagttcttagcagtcctggtactcttgggagtttccatctttctggtctctgc 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3376;
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59.6%; Pred. No. 2.1e-10;
Live 0; Mismatches 74; Indels
SOFTWAKE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 13.8%; Score 64.8; DB 5; Best Local Similarity 57.4%; Pred. No. 8.5e-10; Matches 117; Conservative 0; Mismatches 87;
                                            FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca ESq., Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1242
TELECOMMUICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                   APPLICATION NUMBER: PCT/US94/04496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 cactgcaaccaccgctgcttctac 246
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                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                            LENGTH: 3376 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13,7%
Best Local Similarity 59.6°
Matches 109; Conservative
                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: p-2093 plasmid
US-09-043-303-7
                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 196. 1902
                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION:
PCT-US94-04496-29
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APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Yi
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxla
Patent No. 5741645
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                             ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, STREET: 119 No. 5741645th Fourth Street, Suite 203 CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Orr, Harry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 612-305-1225
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 63.43
Matches 97; Conservative
                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 06-JUN
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                           USA
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US-08-469-802B-5
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Gaps
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APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A. STREET: P.O. Box 581415
CITY: Minneapolis
STATE: M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATE: DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/267,803B FILING DATE: 28-JUN-1994 CLASSIFICATION ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 63.4; DB 2; I
Pred. No. 4.4e-10;
O; Mismatches 56;
                                   221 accactgcaaccaccgctgcttctaccactgct 253
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                                                                                                                                                                             Sequence 4, Application US/08267803B Patent No. 5834183
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US-08-469-802B-5/c
; Sequence 5, Application US/08469802B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: MCCOFMACK, Myra H.
RECISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 612-305-1228
INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 168 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.5
Best Local Similarity 63.4
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 8: CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                          US-08-267-803B-4/C
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                                                                   101 gcccagaatccgacaacagctgctccagctgacacgtatccagctactggtcctgctgat 160
                                                                                                                                     0; Gaps
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Score 63.4; DB 1; Length 171;
Pred. No. 4.4e-10;
0; Mismatches 56; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Type 1 and Method for Diagnosis
                                                                                                                                                                                                          221 accactgcaaccaccgctgcttctaccactgct 253
                                                                                                                                                                                                                                46 GCTGCTGCTGCTGCTGCTGCTGCTGCT 14
                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08267803B Patent No. 5834183 GENERAL INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08469802B
Patent No. 5741645
GENERAL INFORMATION:
APPLICANT: Crt. Harry T.
APPLICANT: Chung, Ming-yi
APPLICANT: Coghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 171;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A. STREET: 119 No. 5741645th Fourth Street, Suite 203 CITY: Minneapolis STATE: MN
                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
F1LING DATE: 28-JUN-1994
CLIASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 63.4; DB 2;
Pred. No. 4.4e-10;
0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 accactgcaaccaccgctgcttctaccactgct 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 GCTGCTGCTGCTGCTGCTGCTGCTGT 14
                                                                                                                                                                                                                                                                                                                                                        110.00030120
                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MCCOFMack, Myra H.
REGIETRATION NUMBER: 36,602
REFRENCE/DOCKET NUMBER: 110.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.5%;
Best Local Similarity 63.4%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 171 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                       ZIP: 55458-1415
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (
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                                                                                            USA
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                                                     CITY: Mi
STATE: M
COUNTRY:
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APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: 20ghbi, Huda Yi
APPLICANT: 20ghbi, Huda Yi
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56; Indels
NYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 63.4; DB 1;
Pred. No. 4.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
                                                                                                                                                                                                   110.00030101
                                                             APPLICATION NUMBER: US/08/469,802B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/08267803B
; Patent No. 5834183
                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFRENCE/CDCKET NUMBER: 110.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.5%;
                                                                                                                                                                                                                                                              TELEFAX: 612-305-1225
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 63.4%;
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: DNA US-08-469-802B-2
                                                                                                                                                                                                                                                                                                                                                                                                   linea
                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEPA: 612-305-1228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
ONLECULE TYPE: DNA
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0;							
Ouery Match 13.5%; Score 63.4; DB 2; Length 195; Best Local Similarity 63.4%; Pred. No. 4.8e-10; Matches 97; Conservative 0; Mismatches 56; Indels 0; Gaps	101 geccagaaleegacaacagetgetecagetgacaegtatecagetactggteetgat 160		161 qatyaagcccctgatgctgaaaccactgctgctgcacaactgcgaccactgctgctcct 220	130 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	221 accactgcaaccaccgctgcttctaccactgct 253	70 GCTGCTGCTGCTGCTGCTGCTGCTGCT 38	
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Search completed: October 5, 2002, 05:08:26 Job time: 4146 sec



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Run on:

Sequence:

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AXX40676 Sequence
BD007429 Reagent a
AX2240677 Sequence
AX079476 Sequence
AX079476 Sequence
AX079478 Sequence
BD007428 Reagent a
AX079842 Homo sapi
AX079842 Homo sapi
AXX40678 Sequence
BD007430 Homo sapi
AX240678 Sequence
AX240678 Sequence
AX240678 Sequence
AX3976 Rat salivar
BD007430 Reagent a
M33976 Rat salivar
BD007430 Reagent a
AX06245 Rattus no
AX0645719 Larus arg
AX045719 Homo sapi
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Continuation (2 of
AC096966 Rattus no
AC092203 Mus muscu
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AX328498
AX067322
AF414087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unclassified.
Unclassified.
1 (bases 1 to 497)
Edwards,J.-B.Dumas.Milne., Duclert,A. and Bougueleret,L.
Complementary DNAs
Patent: US 6312922-A 41 06-NOV-2001;
Location/Qualifiers
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AF139019
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Pred. No. 1.6e-96;
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138 c 90 g
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14.4 98201

14.4 175695

14.3 180668

14.2 173851

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4446.2
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3300.8
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FEATURES
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AR177347
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                                                        5, 2002, 04:00:45; search time 1900.29 Seconds (without alignments) 5186.787 Million cell updates/sec
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                                                                                                 US-09-525-361A-23
471
1 ctttgaagcattttgtctg.....aactatgagcgagctaacat 471
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                        1797656 segs, 10463268293 residues
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Maximum Match 100%
Listing first 45 summaries
                                      - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Perfect score:
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Minimum DB s Maximum DB s

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PAT 31-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                  Gordon, J.,
J., Rapp, L.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C12N5/10,C12P21/02,C12Q1/68,G01N33/53,C12N15/00,C12N5/00, PC
                                             240
 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PN JP 2001503980-A/4
PD 27-MAR-2001
PF 31-OCT-1997 JP 1998520795
PR 31-OCT-1996 US 08/742067
PI PATRICITA A BILLING MEDEL, MAURICE COHEN, TRACY L COLPITTS, POLA N FRIEDMAN,
PI JULIAN GORDON FINANDS " ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
  ttctaccactgctcgtaaagacattccagttttacccaaatgggttggggatctcccgaa
                                                                                                                257 ITCTACCACTGCTCGTAAAGACATTCCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAA
                                                                                                                                       301 tggtagagtgtgtccctgagatggaatcagcttgagtcttctgcaattgggtcacaacta
                                                                                                                                                                                   361 ttcatgcttcctgtgatttcatccaactacttaccttgcctacgatatcccctttatctc
                                                                                                                                                                                               1 (bases 1 to 482)
Medel, PA.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gor
Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D.,
Russell,J.C. and Stroupe,S.D.
Reagent and method useful in detecting mammary diseases
Patent: JP 2001503880-A 4 27-MAR-2001;
ABBOTT LABORATORIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOHN D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL,
                                                                                                                                                                                                                                                                                                       שוו A82 bp DNA linear PAT Reagent and method useful in detecting mammary diseases.
BD007431
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                                                                                                                                                                                                                                           others
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Pred. No. 3.5e-96;
2; Mismatches 2;
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    .482
    /organism~"unidentified"

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136 c 90 g
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                                                                                                                                                                                                                                                                                                                                               BD007431.1 GI:18635802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Topology: Linear;
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                                                                                                                                                                                                                                                                                                                                                         JP 2001503980-A/4.
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PC C12N15/09,A61
PC C12N15/10,C12P
A61K37/02
CC Strandedness:
CC Topology: Lir
FH Key
FT Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 98.9
Matches 458; Conservative
                                                                                                                                                                                                                                                                                                                                                                     unidentified.
unidentified
unclassified.
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PI JOHI
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AUTHORS
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                     1 ctttgaagcatttttgtctgtgctccctgatcttcaggtcaccaccatgaagttcttagc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1;
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Houghton, R.L., Dillon, D.C., Molesh, D.A., Xu, J.,
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Pred. No. 1.6e-96;
J; Mismatches 6;
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Patent: WO 0175171-A 30 11-OCT-2001;
 Mismatches
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Sequence 30 from Patent W00175171.
AX282981
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1. 578
/organism="Homo sapiens"
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137 c 88 a
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98.5%;
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Matches
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LOCUS
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1 (bases 1 to 553)
Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J.,
Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J.,
Russell, J.C. and Stroupes, S.D.
Reagent and method useful in detecting mammary diseases
ABBOTT LABORATORIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61P35/00, C07K14/47, 
C07K16/30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C12N5/10,C12P21/02,C12Q1/68,G01N33/53,C12N15/00,C12N5/00, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
JP 2001503980-A/5
JP 2001503980-A/5
31-OCT-1997 JP 1998520795
31-OCT-1996 US 08/742067
PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACY L COLPITTS, PI
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clttgaagcattttgtctgtgctcctgatcttcaggtcaccaccatgaagttcttagc 60
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detecting mammary
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                                                                                                                                                                                                                                                                                                                   /organism='Unidentified'
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                               and method useful in
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Topology: Linear;
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JP 2001503980-A/5.
unidentified.
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unclassified.
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Bummania: Eutheria: Primates: Catarrhini; Hominidae: Homo.
1 (bases 1 to 472)
Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.
Roberts-Rapp, L., Russell, J.C. and Stroupe, S.D.
Raagents and methods useful for detecting diseases of the breast
Patent: WO 0165262-A 5 07-SEP-2001;
ABBOTT LABORATORIES (US)
                                                                                                                                          Gaps
                                                                                                                                                                                                                            aaccactgctgctgcaacaactgcgaccactgctgctcctaccactgcaaccaccgctgc
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                                                   Score 446.8; DB 6;
Pred. No. 3.9e-96;
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                                                                                0; Mismatches
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/organism="unidentified"
/db_xref="taxon:32644"
144 c 101 q 146
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/db_xref="taxon:9606"
134 c 86 q 144
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AX240679
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98.3%;
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1 (bases 1 to 473)

Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,

Gordon, J., Granados, E. M., Hodges, S.C., Klass, M.R., Kratochvil, J.D.

Roberts-Rapp, L., Russell, J.C. and Stroupe, S.D.

Reagents and methods useful for detecting diseases of the breast Patent: WO 0165262-A 6 07-SEP-2001;
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Pred. No. 5.4e-96;
D; Mismatches 3;
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/db_xref="taxon:9606"
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Sequence 6 from Patent WO0165262.
AX240680 AX240680.1 GI:15797663
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methods of screening for breast cancer
TGCTCCAGCTGACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGA 188
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Catarrhini; Hominidae; Homo,
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Patent: WO 0135811-A 1 25-MAY-2001
EOS Biotechnology, Inc. (US)
Location/Qualifiers
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/organism="Homo saplens"
/db_xref="taxon:9606"
a 132 c 88 g 147
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AX328498
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Mack,D. and Gish,K.C.
Novel methods of diagnosing and
                                                                                                                                                                                                                                                                                                                                      Chordata;
Primates;
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Mammalia; Eutheria;
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nes 469; Conservative
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418
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llarity 98.3%; Pred. No. 4.9e-95;
Conservative 2; Mismatches 5
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CORIXA CORPORATION (US)
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                                                                                                                     AX067322 488 bp
Sequence 26 from Palent WO0078960.
AX067322
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/db_xref="taxon:9606"
129 c 84 g 138
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ETTAAATTATTAAPTTATTAASTTARKDIPVLPKWVGDLPNGRVCP"
117 c 80 g 116 t
PRI 17-SEP-2001
                                                                                                                                                                                                                                                                           2. [bases 1 to 396]
Mikatoek, R.J., Myal, Y., Watson, P.H., Murphy, L.C. and Leygue, E.
Direct Submission
Submitted (23-NG-2001) Biochemistry and Medical Genetics,
University of Manitoba, 770, Bannatyne Avenue, Winnipey, MB R3EOW3,
                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 396)
Miksicek, R. J., Myal, Y., Watson, P. H., Murphy, L.C. and Leygue, E.
Identification and characterization of a novel breast-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="normal breast tissue and breast tumor"
/note="corresponds to SAGE tag: cttcctgtga (Unigene
HS343493)"
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/note="SBEM; secreted protein; similar to
linear
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/protein_id="AAL02119.1"
/db_xref="G1:15559111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 383.4; DB 9;
Pred. No. 4.8e-81;
0; Mismatches 1;
mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
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1. .396
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Best Local Similarity 99.5%;
Matches 395; Conservative (
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Unpublished
AF414087
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C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61P35/00, C07K14/47,
C07K16/30,
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     Rapp, L.R.
                                                                                                                                                                                                                        C12N5/10,C12P21/02,C12Q1/68,G01N33/53,C12N15/00,C12N5/00, PC
Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, IRussell, J.C. and Stroupe, S.D.
Reagent and method useful in detecting mammary diseases
Patent: JP 2001503980-A 2 27-MAR-2001;
Subject LABORATORIES
OS Unidentified
PN JP 2001503980-A/2
PP 27-MAR-2001
PP 31-OCT-1990 JP 1998520795
PR 31-OCT-1996 US 08/742067
PP PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACY L COLPITTS, I
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JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, PI
                                                                                                                                                                        JOHN D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL,
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                                                                                                                                                                                                                                                                                                                                                                                                          63.9%; Score 300.8; DB 6; Length 308; 99.3%; Pred. No. 2.2e-61; ive 0; Mismatches 2; Indels 0;
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/organism="unidentified"
/db_xref="taxon:32644"
a 94 c 65 g 87
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Sequence 3 from Patent W00165262.
AX240677
AX240677.1 GI:15797660
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synthetic construct
artificial sequence.
1 (bases 1 to 292)
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STEVEN D STROUPE
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PC C07K1
PC C12N5
A61K37/02
CC Stran
CC Topol
FH Key
FT Sourc
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AX240677
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                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(bases 1 to 308)
Billing Medel.P.A., Cohen,M., Colpitts,T.L., Friedman,P.N.,
Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D.,
Roberts-Rapp,L., Russell,J.C. and Stroupe,S.D.
Reagents and methods useful for detecting diseases of the breast
ABHOOT LABORATORIES (US)
                                                                                                PAT 26-SEP-2001
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Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
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63.9%; Score 300.8; DB 6;
Best Local Similarity 99.3%; Pred. No. 2.2e-61;
Malches 302; Conservative 0; Mismatches 2;
         DNA
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                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
94 c 65 g 86
                                                                                             AX240676 308 bp
Sequence 2 from Patent WO0165262.
AX240676
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                                                                                                                               AX240676.1 GI:15797659
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JP 2001503980-A/2.
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AX240676
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Homo sapiens
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Best Local S
Matches 258
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AX079476
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Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Roberts-Rapp, L., Russell, J.C. and Stroupe, S.D. Reagents and methods useful for detecting diseases of the breast, Abatent: WO 0165262-A 3 07-SEP-2001; ABBOTT LABORATORIES (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mack, D. and Gish, K.C. Novel methods of diagnosing and determining prognosis of breast cancer. compositions, and methods of screening for breast cancer
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                                                                                                                                                                                                                                                                                                                                                                      Length 292;
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99.3%; Pred. No. 5.1e-54;
iive 0; Mismatches 2;
                                                                                  /organism="synthetic construct"
/db_xref="taxon:32630"
/note="EST Clone 901429"
92 c 59 9 80 t
                                                                                                                                                            Score 286.8; DB 6
Pred. No. 4.6e-58;
0; Mismatches 4
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Patent: WO 0135811-A 2 25-MAY-2001;
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/db_xref="taxon:9606"
85 c 59 g 71
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AX328499
AX328499.1 GI:18098425
                                                                  Location/Qualifiers
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Location/Qualifiers
                                                                                                                                                           60.98;
98.68;
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Best Local Similarity 98.6°
Matches 288; Conservative
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Matches 271;
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226
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Baker, K.P., Goddard, A. and Wood, W.I.
Human polypeptides and methods for the use thereof Patent: WO 0107611-A 220 01-FEB-2001; Genentech, Inc. (US)
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                    Homo sapiens
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini: Hominidae; Homo.
1 (bases 1 to 266)
Haker, K. P., Goddard, A. and Wood, W.I.
Human polypeptides and methods for the use thereof
Patent: WO 0107611-A 219 01-FEB-2001;
Genentech, Inc. (US)
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Breast cancer; diagnosis; prognosis; detection; screening; antibody; oestrogen receptor; anti-oestrogen; immune response; lymph node; metastases; tumour; BCR3; BCQ8; BCQ5; BCH1; BCN1; BCN2; BCN5; BCN2; BCN2; BCN3; BCN3; BCR2; BCN3; BC
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Exons D, C, B and

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                                                                                                                                                                                                                                         comprise adding a drug candidate to a cell that expresses a protein selected from BCH1, BCA2, BCJ7, BCN1, BCN5, BCO2, BCO5, BCC8, BCR2, and BCY3 or their fragments and determining the effect of the drug on the expression of those proteins. Antibodies to breast cancer genes (specifically BCH1 or its fragment (BCH1p1 or BCH1p2)) are useful for inhibiting and treating breast cancer in individuals who are non-responsive to anti-oestrogen and positive for oestrogen receptor. Compositions comprising BCH1 or a nucleic acid encoding in BCH1 are useful for eliciting an immune response in an individual. The antibodies are also useful for the diagnosis and prognosis of breast cancer and for screening compositions which modulate the breast cancer phenotype. The method allows rapid and simple
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                                                                       (EOSB-) EOS BIOTECHNOLOGY INC
99US-0440676.
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The present sequence encodes a human breast cancer protein, designated BCH1. BCH1 is upregulated in breast cancer tissue, and is found on chromosome 12. Cytoband 12q12. BCH1 can be used as an indicator of breast cancer, for determining non-responsiveness to anti-oestrogen therapy and for treating breast cancer. BCH1 nucleic acid is useful for day and single breast cancer, and BCH1 is useful for determining the prognosis of breast cancer and for determining whether an individual with breast cancer will be responsive to anti-oestrogen therapy (where the prognosis and non-responsiveness, respectively. BCH1 is also useful for screening for candidate drugs and bloactive agents. Inhibitors, contibodies and antisense sequences of BCH1 are useful for treating breast cancer. Antibodies to BCH1 are useful for localizing a therapeutic moiety (e.g. cytocoxic agent or radioisotope) to breast cancer tissue, and for treating breast cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes and protein useful for the diagnosis and treatment of breast
                                                                                                    Nucleotide sequence of a human breast cancer protein designated BCH1.
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                                                                                                                                   protein; BCH1; breast cancer; chromosome 12; 12q12;
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Pred. No. 3.4e-119;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                  "breast cancer protein BCH1"
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                                                                                                                                                                                                          Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 73pp; English.
                BP.
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             AAF85500 standard; cDNA; 471
                                                                                                                                                                                                                                                                                                                                                                                                   99US-0440676.
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                                                                        (first entry)
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Matches 470; Conservative
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/*tag=
                                                                                                                                               anti-oestrogen therapy;
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                                                                                                                                   cancer
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                                                                      23-JUL-2001
                                                                                                                                                                                                                                                                   sig_peptide
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                                           AAF85500;
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                                                                                                                                                                            in vaccines for immunotherapy,
    tgytagagtgtgtccctgagatggaatcagcttgagtcttctgcaattgggtcacaacta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; immunogenic fragment; vaccine; detection;
development; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                              human breast tumour protein immunogenic fragment.
                                                                                                                                                                                                                                                                    breast tumour protein genes used,
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97US-0998253.
97US-0998255.
98US-0118554.
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24-DEC-1997
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manufacture of a medicament for treating breast cancer in a patient. Antigen presenting cells incubated in the presence of at least one polypeptide are also useful for treating breast cancer.
                                                                                              agtcctggtactcttgggagtttccatctttctggtctctgcccagaatccgacaacagc
                                                                                                                                                                                                              aaccactgctgctgcaactgcgaccactgctgctcctaccactgcaaccaccgctgc
                                                                                                                                                                         tgctccagctgacacgtatccagctactggtcctgctgatgatgaagcccctgatgctga
                                                                                  <u>.</u>;
                                                                 Length 480;
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                                  Sequence 480 BP; 121 A; 132 C; 87 G; 140 T; 0 other;
                                                               Score 448.4; DB 20;
Pred. No. 2e-113;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA sequence of human breast tumour clone 1016F8.
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                                                             Query Match 95.2%;
Best Local Similarity 98.5%;
Matches 463; Conservative
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breast cancer;
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                                                                                             The present sequence was isolated from a breast tumour cDNA library. It is provided in a specification relating to compounds for immuncherapy and diagnosis of breast cancer. Breast tumour antigens and the polynucleotides that encode them may be used in the production of a pharmaceutical composition to be used in the treatment of breast cancer. Proliferated T cells and incubated antigen presenting cells are also required. The polypeptides and polynucleotides may also be used to
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breast
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                                                                                                                                                                                                                       Sequence 480 BP; 121 A; 132 C; 87 G; 140 T; 0 other;
                               detection and
                                                                                                                                                                                                                                                                     Score 448.4; DB 21;
Pred. No. 2e-113;
H: Mismatches 6;
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              novel isolated polypeptide comprising
                               the
                               breast cancer protein useful in
                                                                     Claim 4; Page 74; 95pp; English.
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98.5%;
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                                                                                                                                                                                                                                                                                               463; Conservative
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endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                               encode
                                                                                                                                                                                                                                                                                                                                                                                            sequence represents a nucleic acid molecule which encodes a
                                                                                                                                                                                                                                                                                                                                                    diagnosis and treatment of e.g. cancers, neurological immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                           New isolated human genes and the secreted polypeptides they useful for diagnosis and treatment of e.g. cancers, neurolog
                                                                                                                                                                                                                                                                                      Florence KA;
Ni J, Olse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 489 BP; 124 A; 134 C; 91 G; 140 T; 0 other;
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Moore PA,
                                                                                                                                                                                                                                                                                           DW, Muc.
Young P;
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1, Shi Y,
                                                                                                                                                                                                                                                                                       Ebner R,
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97US-0048069
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97US-0048154.
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Ruben SM,
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                 Homo sapiens.
                                W09842738-A1
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-MAY-1997;
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21-MAR-1997
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Indels

Length 489;

DB 20;

Similarity 98.5%; Score 448.4; DB 20; Similarity 98.5%; Pred. No. 2e-113; 3; Conservative 0; Mismatches 6;

Best Local Sim Matches 463;

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Query Match

ctttgaagcatttttgtctgtgctccctgatcttcaggtcaccaccatgaagttcttagc 60

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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foctal deficiency; blood; allergy; renal; ds; inflaumation; ischaemic soften, happen, hood; allergy; renal; ds; inflaumation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; esteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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                                                                                                 tggtagagtgtgtccctgagatggaatcagctlgagtcttctgcaattgggtcacaacta
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                                                                                                                                                                                                                                  secreted protein; fusion protein; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                secreted protein gene 34 clone HMQAJ64.
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97US-0041277.
97US-0041281.
97US-0042344.
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970S-0048094.
970S-0048095.
970S-0048099.
970S-0048131.
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97US-0048186.
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21 - MAR - 1997
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30 - MAY - 1997
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This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin protein as compared to the human protein only.

The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX00611-x00724; amino acid sequences AAX00611-x00724; amino acid sequences AAX00611-x00724; amino acid sequences and which are seful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 87 polypucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agtcctggtactcttgggagtttccatctttctggtctctgcccagaatccgacaacagc 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human genes and the secreted polypeptides they encounseful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20; Length 489;
                                                                                                                                              Florence KA;
Ni J, Olsen HS;
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Pred. No. 2e-113;
0; Mismatches (
                                                                                                                                             Ebner R, Ferrie AM,
Lafleur DW, Moore PA,
, Shi Y, Young P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for described uses).
                                                                                                                                                                                                                                                                                                Claim 1; Page 198; 385pp; English.
                97US-0048188.
97US-0048350.
97US-0048351.
97US-0048352.
97US-0048355.
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ilarity 98.5%;
Conservative 0
                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                     97us-0054804
                                                                                                                                                                      Ruben SM,
                                                                                                                                           Duan R,
                                                                                                                                                                                                  MPI; 1999-070066/06
                                                                                                                                                          Hu JS,
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30-MAY-1997;
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30-MAY-1997;
30-MAY-1997;
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05-AUG-1997;
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Matches 463; (
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This sequence encodes a human secreted protein of the invention. The extended cDNAs (or genomic DNAs obtainable from them) may be used to prepare PCR parimers and probes. These are useful for forensic matching or positive identification by DNA sequencing. They may also be used in the positive identification by DNA sequencing. They may also be used in the positive identification of the extended cDNAs are useful in identification of proteins encoded by the extended cDNAs are useful in identification of tissue types or cell species, as well as identifying tissue specific collentification of genes associated with hereditary diseases or drug response. Signal sequences can be used for chromosome mapping and constitution of secretion vectors. Other sequences derived from the extended cDNAs can be used in construction of secretion vectors. Other sequences derived from the extended cDNAs can be used to clone upstrame genomic DNA sequences including promoters. This is in turn useful for identifying proteins may be useful in diagnosing and treating several disorders including, but not limited to: cancer, hyperlipidaemia, cardiovascular and neurodegenerative disorders, autoimmune diseases, and mino acidurias, hypoglycaemia, male rat infertility and myopathies.
                                                                                                                                                                                                                                                           Secreted protein; fingerprint identification technique; chromosome mapping; human; hereditary disease; diagnosis; cancer; hyperlipidaemia; cardiovascular; neurodegenerative disorder; therapy; autoimmune disease; rheumatic disease; embryogenic disorder; myopathy; renal lnjury; amino aciduria; hypoglycaemia; male rat infertility; hypertension; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to obtain
and
                                                                                                                                                                                                                                         Secreted protein EST coding sequence 108-002-5-0-F3-FL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bougueleret L, Duclert A, Dumas Milne Edwards J;
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98US-0081563.
98US-0096116.
98US-0099273.
                                                                                                                             AA240783 standard; DNA; 497
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The present sequence was isolated from a breast tumour cDNA library. It is provided in a specification relating to compounds for immunotherapy
                                                                                                                                                                                                        tggtagagtgtgtccctgagatggaatcagcttgagtcttctgcaattgggtcacaacta 360
                                                                                                                                                                                                                                     ttcatgcttcctgtgatttcatccaactacttaccttgcctacgatatcccctttatctc 420
                                                                                                                                                                                                                                                A novel isolated polypeptide comprising an immunogenic portion of a breast cancer protein useful in the detection and treatment of breast cancer.
                                    tgctccagctgacacgtatccagctactggtcctgctgatgatgatgaagccctgatgctga
 ctttgaagcatttttgtctgtgctccctgatcttcaggtcaccaccatgaagttcttagc
                                                                                              tgctccagctgacacgtatccagctactggtcctgatgatgaagcccctgatgctga
                                                                                                                  aaccactgctgctgcaacaactgcgaccactgctgctcctaccactgcaaccaccgctgc
                                                                                                                                                         ttctaccactgctcgtaaagacattccagttttacccaaatgggttggggatctcccgaa
                                                                                                                                                                                                                                                                            Human; breast tumour antigen; cytostatic; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequence of human breast tumour clone B511S.
                                                                                                                                                                                                                                                                                                                                                BP.
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                                                                                                                                                                                                                                                                                                                                              AAC79470 standard; cDNA; 578
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02-JUL-1999;
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Indels

Length 497;

Score 448.4; DB 20; Pred. No. 2e-113; 0; Mismatches 6;

95.2%; 98.5%;

Best Local Similarity 98.5 Matches 463; Conservative

Query Match

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        polynucleotides that encode them may be used in the production of a pharmaceutical composition to be used in the treatment of breast cancer. Proliferated T cells and incubated antigen presenting cells are also required. The polypeptides and polynucleotides may also be used to produce a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetic subtraction; DNA microarray analysis; polymerase chain reaction; cancer; B5115; ss.
                                                                                                                                                        tgctccagctgacacgtatccagctactggtcctgctgatgatgaagcccctgatgctga 180
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    and the
                                                                                        DB 21; Length 578;
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and diagnosis of breast cancer. Breast tumour antigens
                                                            88 G; 147 T; 0 other;
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                                                                                      Score 448.4; DB 21,
Pred. No. 2.2e-113;
0; Mismatches 6;
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63..335
                                                            Sequence 578 BP; 206 A; 137 C;
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Best Local Similarity 98.5%;
Matches 463; Conservative 0
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The invention relates to identifying tissue-specific polynucleotides (P) from that involves performing a genetic subtraction to identify pool of (P) from tissue of interest (T1), performing DNA microarray analysis to identify first subset of polynucleotides (SP1) at least 2-fold over expressed in T1, and performing quantitative polymerase chain reaction (PCR) analysis on SP1 to identify second aubset of (P). The method is useful for determining the presence or absence of a cancer cell in a patient, monitoring the progression of cancer in a patient using a biological sample such as blood, serum, lymph nodes, bone marrow, sputum, the presence or absence of or monitoring progression of prostate, breast, the presence or absence of or monitoring progression of prostate, breast, colon, covarian, lung, head and neck, lymphoma, leukemia, melanoma, liver, squartic, kidney, bladder, pancreatic or endometrial cancer. The present segent
                                                                                                                                               Identifying tissue (tumour)-specific polynucleotides overexpressed in tissue of interest as compared to control tissue, for detecting cancercells in patient, comprises DNA microarray analysis or quantitative
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98.5%; Pred. No. 2.2e-113;
live 0; Mismatches 6;
                                                                                  Xu J,
                                                                                  DA,
                                                                                                                                                                                                                 Claim 4; Page 116; 127pp; English.
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20-JUL-2000; 2000US-219862P.
27-JUL-2000; 2000US-221300P.
18-DEC-2000; 2000US-256592P.
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                                                                                                                                                                                                                                                                                                                       BS106 is a breast tissue gene with which breast cancer and related, diseases are associated. The BS106 polynucleotides AAV31989-V31993 can be detected by BS106 specific polynucleotides or complements acting as useful markers for detection methods. The products and methods can be used for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast such
                                                                                      ss; human; BS106; breast tissue gene; breast cancer; detection marker.
                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                       Detecting BS106 gene products - useful for developing products detecting, staging, preventing, treating or determining predisposition to e.g. breast cancer
                                                                                                                                                                                                                    Friedman PN;
MR, Kratochvil
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 482 BP; 109 A; 136 C; 90 G; 145 T; 2 other;
                                                                                                                                                                                                                 Cohen M, Colpitts TL,
s EN, Hodges SC, Klass
ussell JC, Stroupe SD;
                                                                        sednence.
                                                                                                                                                                                                                                                                                                        Claim 1; Page 88; 114pp; English.
                                                                     BS106 polynucleotide consensus
                  DNA; 482 BP
                                                                                                                                                                                                                                   Russell JC,
                                                                                                                                                              97WO-US19836
                                                                                                                                                                               96us-0742067
                                                    (first entry)
                                                                                                                                                                                                                            Granados EN,
                                                                                                                                                                                                                                                     WPI; 1998-272234/24.
                                                                                                                                                                                                (ABBO ) ABBOTT LAB.
                 AAV31992 standard;
                                                                                                                                                                                                                 Billing-Medel PA,
                                                                                                                                                                                                                                                                                                                                                                                breast cancer.
                                                                                                                                                                                                                                   Roberts-Kapp L,
                                                                                                         Homo sapiens.
                                                                                                                           WO9818945-A1.
                                                                                                                                                           31-OCT-1997;
                                                   25-SEP-1998
                                                                                                                                                                              31-0CT-1996;
                                                                                                                                            07-MAY-1998.
                                  AAV31992;
10
         AAV31992
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Friedman PN;

Colpitts TL, Fr SC, Klass MR, Stroupe SD;

Granadose, Hodges Cohen M,

WPI; 1999-326991/27.

P-PSDB; AAY13466 Roberts-rapp L,

98WO-US22020.

19-OCT-1998; 31-OCT-1997;

14-MAY-1999

97US-0962094.

(ABBO ) ABBOTT LAB Billiing-Medel PA, New isolated BS106 nucleic acids

BS106; breast; marker; detection; diagnosis; breast cancer;

Homo sapiens. W09923230-A1

BS106 consensus polynucleotide sequence.

(first

26-JUL-1999

AAX55581;

AAX55581 standard; DNA; 482

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Sequences AAX55578-82 represent overlapping polynucleotide sequences of BS106 clones isolated from the breast tissue. The BS106 nucleic acids correspond to a breast tissue gene and can be used as markers for breast tissue disease. The products can be used for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining diseases or conditions associated with BS106, especially
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                       ::
                                                                                                                                                                                                   Length 482;
                                                                                                                                                                                                                             Indels
                                                                                                                                                Sequence 482 BP; 109 A; 136 C; 90 G; 145 T; 2 other;
                                                                                                                                                                                              Score 447; DB 20;
Pred. No. 4.9e-113;
2; Mismatches 2;
Claim 11; Page 89; 105pp; English.
                                                                                                                                                                                                94.98;
98.98;
                                                                                                                                                                                           Query Match
Best Local Similarity 98.9°
Matches 458; Conservative
                                                                                                                    breast cancer
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                                                                                                                                                                                                                                                                                                                                                                                                 tggtagagtgtgtccctgagatggaatcagcttgagtcttctgcaattgggtcacaacta 360
                                                                      Gaps
                                                                                            aaccactgctgctgcaacaactgcgaccactgctgctcctaccactgcaaccaccgctgc
                                                                      ä
                                 Ouery Match
94.9%; Score 447; DB 19; Length 482;
Best Local Similarity 98.9%; Pred. No. 4.9e-113;
Matches 45%; Conservative 2; Mismatches 2; Indels
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BS106 is a breast tissue gene with which breast cancer and related: diseases are associated. The BS106 polynucleotides AAV31989-V31997 can be detected by BS106 specific polynucleotides or complements acting as useful markers for detection methods. The products and methods can be used for detecting, diagnosing, staging, preventing or treating or determining predisposition to diseases or conditions of the breast such as breast cancer.
                                                                                                                                                                                                                                                                                                  ss; human; BS106; breast tissue gene; breast cancer; detection marker.
                                   257
                                                                            Lggtagagtgtqtccctgagatggaatcagcttgagtcttctgcaattgggtcacaacta 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting BS106 gene products - useful for developing products detecting, staging, preventing, treating or determining predisposition to e.g. breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                            Friedman PN;
MR, Kratochvil
                                                                                                                                                    Sequence 553 BP; 159 A; 144 C; 101 G; 148 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Colpitts TL,
jes SC, Klass
                                                                                                                                                                                                                                                                               BS106 polynucleotide clone 1662885 (ii).
                                                                                                                                                                                                                                                                                                                                                                                                                          Billing-Medel PA, Cohen M, Colpitts .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 90; 114pp; English.
                                                                                                                                                                                                                          ВР
                                                                                                                                                                                                                         DNA; 553
                                                                                                                                                                                                                                                                                                                                                                                 97WO-US19836.
                                                                                                                                                                                                                                                                                                                                                                                                   96US-0742067.
                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                      AAV31993 standard;
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                                                                                                                                                                                                                                                             25-SEP-1998
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Sequences AAX55578-82 represent overlapping polynucleotide sequences of BS106 clones isolated from the breast tissue. The BS106 nucleic acids correspond to a breast tissue gene and can be used as markers for breast tissue disease. The products can be used for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining diseases or conditions associated with BS106, especially
                    151
                                                                                          271
                                                                                                                 tictaccacigcicglaaagacaticcagiiittacccaaaigggiigggaiileccgaa
                                                                                                                                           tggtagagtgtgtccctgagatggaatcagcttgagtcttctgcaattgggtcacaacta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colpitts TL, F. SC, Klass MR, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                 BS106 consensus polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 89; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated BS106 nucleic acids
                                                                                                                                                                                                                                                                               ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lose, Hodges
Russell JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cohen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0962094.
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                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                             AAX55582 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Granadose,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Billiing-Medel PA,
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                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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Indels

DB 19; Length 553;

94.9%; Score 446.8; DB 19. 98.3%; Pred. No. 5.9e-113; iive 0; Mismatches 7;

Conservative

Best Local Similarity Matches 462; Conserv

Query Match

G; 148 T; 1 other;

breast

Score 446.8; DB 20; Pred. No. 5.9e-113; 0; Mismatches 7;

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Human breast specific gene clone Mam002.
         Sequence 553 BP; 159 A; 144 C; 101
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                       tch 94.9%; al Similarity 98.3%; 462; Conservative (
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                                                                                                                                                                                                                                                                                                                 (DIAD-) DIADEXUS LLC
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                                                                                                                                                                                                                                                                                                                           Recipon H,
                                                                                                                                                                                                                                                         breast cancer;
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                       Query Match
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                            Best Local
Matches 46
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This sequence represents a breast specific gene (BSG) clone. The BSG sequences are also referred to as breast specific markers (BSM). The invention relates to methods for diagnosing, monitoring, staging, inaging and treating breast cancer (BC). The methods comprise measuring the levels of BSG products in cells, tissues or body fluids of the patient and comparing the measured levels of BSG, with BSG levels of a normal human control. An antibody against the BSG sequences can be labelled and used for imaging BC in a patient. The antibody can be conjugated to a cytotoxic agent, and used for treating BC in a patient.
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                                                                                                                                                                                                                                                                                      241 ttctaccactgctcgtaaagacattccagttttacccaaatgggttggggatctcccgaa
                                                                                                                                                                                         ::
                                                                                                                                                                     544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; BS106 protein; breast cancer; metastasis; gene therapy; tumour; expressed sequence tag; EST; ss.
                                                                                                                                                                    Score 446.4; DB 21; Length Pred. No. 7.5e-113; 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 544 BP; 142 A; 143 C; 94 G; 154 T; 11 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human BS106 gene-specific full length cDNA,
                  Claim 7; Page 38; 45pp; English.
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                                                                                                                                                                   Similarity 98.5%; 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD18673 standard; cDNA; 472
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                                                                                                                                                                   Query Match
Best Local Simi
Matches 461;
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                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            breast specific gene; breast specific marker; BSG; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting, diagnosing, monitoring, staging, prognosticating, imaging and treating breast cancer using protein product of breast specific
                                             Length 553;
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gene or its fragment which codes for a BS106 polypeptide, useful for ne detection of a breast disease such as breast cancer - \,
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Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                             The invention relates to human BS106-specific polypeptides and polynucleotides. The BS106 polypeptides and antibodies are useful for detecting, diagnosing, staging, monitoring, prognosticating, frequenting, treating or determining the predisposition of an individual to diseases and conditions of the breast such as breast enforcer. They are also useful in the treatment of tumours or metastases. Polynucleotides of the invention are useful in drug screening and gene therapy. The present sequence is human BS106 gene specific full length CDNA, expressed sequence tag (EST) clone
                                                                                                                                                                                                                                                                                                                                                             94.7%; Score 446.2; DB 22; Length 472; ilarity 99.1%; Pred. No. 8e-113; Conservative 0; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                                                                                           Sequence 472 BP; 108 A; 134 C; 86 G; 144 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 1; 158pp; English
28-FEB-2001; 2001WO-US06516
                     29-FEB-2000; 2000US-0516444
                                                                                                                WPI; 2001-596773/67.
                                            (ABBO ) ABBOTT LAB.
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Best Local Similarity
Matches 459; Conserv
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